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Fig. 6

Comparison of amino acid sequences "stripped-down" version of chimera, known as "PigKS" (also called "Pig-Lys") vs. Pig uricase

Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Pig uricase:

Pig cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1601 Length: 319
Ratio: 5.249 Gaps: 0
Percent Similarity: 99.672 Percent Identity: 99.344

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

pigKS.pep x Pig.pep June 25, 1998 17:11 ..

```

pigKS  1  MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGYHSIKEVATSVQLT  50
      |||
Pig    1  MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGYHSIKEVATSVQLT  50
      |||
151  LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS  100
      |||
151  LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIETFAVTICEHFLS  100
      |||
101  SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP  150
      |||
101  SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP  150
      |||
151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||
151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||
201  QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGLGQV  250
      |||
201  QGRDVDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGLGQV  250
      |||
251  PEIEDMEISLPNIHYLNIDMSKMGLINKKEVLLPLDNPYGAITGTVKRKL  300
      |||
251  PEIEDMEISLPNIHYLNIDMSKMGLINKKEVLLPLDNPYGRITGTVKRKL  300
      |||
301  SSRL* 305
      |||
301  TSRL* 305
  
```

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Fig. 7

Comparison of amino acid sequences of the "original" Pig-baboon chimeric uricase ("chimera") with that of the "stripped-down" version of chimera, known as "PigKS" (also called "Pig-Lys")

"Chimera" uricase:

Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to 915 (end)

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

[GCG GAP program]

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1589	Length:	319
Ratio:	5.210	Gaps:	0
Percent Similarity:	98.689	Percent Identity:	98.689

Match display thresholds for the alignment(s):

```

| = IDENTITY
. = 2
. = 1

```

chimera.pep x pigKS.pep June 25, 1998 16:15 ..

```

chim. 1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
      |||
PigKS 1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGKYHSIKEVATSVQLT 50
      |||
151 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGKSIETFAVTICEHFLS 100
      |||
151 LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGKSIETFAVTICEHFLS 100
      |||
161 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP 150
      |||
161 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAFIYTPGTGTHFCEVEQIRNGP 150
      |||
151 FVIHSGIKDLKVLKTTQSGFEGFIKQFTTLPEVKDRCFATQVYCKWRYH 200
      |||
151 FVIHSGIKDLKVLKTTQSGFEGFIKQFTTLPEVKDRCFATQVYCKWRYH 200
      |||
201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
      |||
201 QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTLLGQV 250
      |||
251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNFYGKITGTGVRKRL 300
      |||
251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNFYGKITGTGVRKRL 300
      |||
301 SSRL* 305
      |||
301 SSRL* 305

```

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Fig. 8

Comparison of amino acid sequences of the "original" Pig-baboon chimeric uricase ("chimera") with that of Pig uricase

"Chimera" uricase:

Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to 915 (end)

Pig uricase:

Pig cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 1583 Length: 305
Ratio: 5.190 Gaps: 0
Percent Similarity: 98.361 Percent Identity: 98.033

Match display thresholds for the alignment(s):

```

| = IDENTITY
. = 2
: = 1

```

chimera.pep x Pig.pep June 25, 1998 16:54 ..

```

chim  1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGGKYHSIKEVATSVQLT  50
      |||||
Pig   1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLHIQRDGGKYHSIKEVATSVQLT  50
      |||||
151  LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGKSIETFAVTICEHFLS  100
      |||||
151  LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGKSIETFAVTICEHFLS  100
      |||||
101  SFKHVIRAQVYVEEVPWKRFEKNGVKVHAFIYPTGTGTHFCEVEQIRNGP  150
      |||||
101  SFKHVIRAQVYVEEVPWKRFEKNGVKVHAFIYPTGTGTHFCEVEQIRNGP  150
      |||||
151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||||
151  PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH  200
      |||||
201  QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV  250
      |||||
201  QGRDVFDEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTLCQV  250
      |||||
251  PEIEDMEISLPNIHYFNIDMSKMGLINKKEEVLLPLDNPYGKATGTGTVKRKL  300
      |||||
251  PEIEDMEISLPNIHYFNIDMSKMGLINKKEEVLLPLDNPYGRITGTGTVKRKL  300
      |||||
301  SSRL* 305
      |||||
301  TSRL* 305

```